



SEQUENCE LISTING

<120> Allen, Keith D.
Zhang, Qin

<120> TRANSGENIC MICE CONTAINING CX2 GENE
DISRUPTIONS

<130> R-716

<140> US 09/900,518

<141> 2001-07-06

<150> US 60/216,178

<151> 2000-07-06

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2490

<212> DNA

<213> Mus musculus

<400> 1

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<210> 2

<211> 764

<212> PRT

<213> Mus musculus

<400> 2

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Glu Glu Pro Asp Tyr Tyr Ser Gln Glu Leu Trp Arg Arg Gly Arg Tyr
35     40     45
Tyr Gly His Pro Glu Pro Glu Pro Glu Pro Glu Leu Phe Ser Pro Ser
50     55     60
Met His Glu Asp Leu Arg Val Glu Glu Gln Glu Gln Gln Glu Pro His
65     70     75     80
Gln Gln Gly His Arg Thr Pro Lys Lys Ala Ile Lys Pro Lys Lys Ala
85     90     95
Pro Lys Arg Glu Lys Leu Val Ala Glu Thr Pro Pro Pro Gly Lys Asn
100    105    110
Ser Asn Arg Lys Gly Arg Arg Ser Lys Asn Leu Glu Lys Ala Ala Ser
115    120    125
Asp Asp His Gly Val Pro Val Ala His Glu Asp Val Arg Glu Ser Cys
130    135    140
Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln Leu His
145    150    155    160
Ala Ser Thr Ser Lys Arg Tyr Gly Leu Gly Ala His Arg Gly Arg Leu
165    170    175
Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr Asp Gly Ala Trp
180    185    190
Cys Ala Gly Arg Asn Asp Leu His Gln Trp Ile Glu Val Asp Ala Arg
195    200    205
Arg Leu Thr Lys Phe Thr Gly Val Ile Thr Gln Gly Arg Asn Ser Leu
210    215    220
Trp Leu Ser Asp Trp Val Thr Ser Tyr Lys Val Met Val Ser Asn Asp
225    230    235    240
Ser His Thr Trp Val Thr Val Lys Asn Gly Ser Gly Asp Met Ile Phe
245    250    255
Glu Gly Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val
260    265    270
Pro Met Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp
275    280    285
Asn Gly Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro
290    295    300
Asp Pro Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp
305    310    315    320
Asp Leu Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met
325    330    335
Lys Val Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile
340    345    350
Gly Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
355    360    365

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His	Pro	Gly	Glu	His	Glu	Val	Gly	Glu	Pro	Glu	Phe	His	Tyr	Ile	Ala
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385				390						395					400
Leu	His	Phe	Leu	Cys	Gln	Glu	Tyr	Ser	Ala	Gln	Asn	Ala	Arg	Ile	Val
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Asp	Gly	Tyr	Glu	Lys	Ala	Tyr	Glu	Gly	Gly	Ser	Glu	Leu	Gly	Gly	Trp
		435					440					445			
Ser	Leu	Gly	Arg	Trp	Thr	His	Asp	Gly	Ile	Asp	Ile	Asn	Asn	Asn	Phe
	450					455					460				
Pro	Asp	Leu	Asn	Ser	Leu	Leu	Trp	Glu	Ala	Glu	Asp	Gln	Gln	Asn	Ala
465					470					475					480
Pro	Arg	Lys	Val	Pro	Asn	His	Tyr	Ile	Ala	Ile	Pro	Glu	Trp	Phe	Leu
				485					490					495	
Ser	Glu	Asn	Ala	Thr	Val	Ala	Thr	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp
		500						505					510		
Met	Glu	Lys	Ile	Pro	Phe	Val	Leu	Gly	Gly	Asn	Leu	Gln	Gly	Gly	Glu
	515						520					525			
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Gln	Glu	His	Thr	Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala
545					550					555					560
Tyr	Ser	Tyr	Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg
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Ala	Ser	Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu
		595				600						605			
His	Thr	Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys	Tyr
	610					615					620				
Pro	His	Glu	Ser	Glu	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg	Glu	Ser
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				645					650					655	
Arg	Asp	Leu	Gln	Gly	Lys	Gly	Ile	Ser	Asn	Ala	Val	Ile	Ser	Val	Glu
		660						665					670		
Gly	Val	Asn	His	Asp	Ile	Arg	Thr	Ala	Ser	Asp	Gly	Asp	Tyr	Trp	Arg
		675					680					685			
Leu	Leu	Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr	Ala	Lys	Ala	Glu	Gly	Phe
	690					695					700				
Ile	Thr	Ser	Thr	Lys	Asn	Cys	Met	Val	Gly	Tyr	Asp	Met	Gly	Ala	Thr
705				710						715					720
Arg	Cys	Asp	Phe	Thr	Leu	Thr	Lys	Thr	Asn	Leu	Ala	Arg	Ile	Arg	Glu
				725					730					735	
Ile	Met	Glu	Thr	Phe	Gly	Lys	Gln	Pro	Val	Ser	Leu	Pro	Ser	Arg	Arg
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<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting Vector

<400> 3

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caggagctct ggcggcgcgg gcgctattat gggcatccgg agcctgagcc ggagccggag 180
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<210> 4

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting Vector

<400> 4

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tgagcccagc caaagtcctg tggcgctgtg gttattccct agagactaca tctgagctaa 180
gttcagcttt ctctccctgc                                     200

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